Biocomplexity of Introduced Avian Diseases in Hawaii: Threats to Biodiversity

Palila. Photo courtesy of C.M. Atkinson, USGS.

Biological invasions involve complex interactions over a wide range of temporal and geographic scales. These invasions are becoming more frequent, are widely distributed throughout the world, and can pose a significant threat to biological diversity.

The Hawaiian Islands are particularly well suited for investigating these invasion processes because of their relative isolation and because their complex topography creates wide variability in climate and habitats across limited geographic areas. These conditions facilitate studies of the interactions of a wide range of biotic and abiotic factors on the invasion process over spatial scales that are orders of magnitude less than in most continental areas.

Accidental introduction of mosquito-borne avian malaria and pox virus to Hawaii is an outstanding example of how biological invasions can have a profound effect on endemic biota. The geographic distribution, density, and community structure of endemic Hawaiian avifauna has changed dramatically in the last century, in large part because of the spread of these diseases and their introduced mosquito vector. This disease system is dynamic and biologically complex, involving both direct and indirect interactions among endemic and introduced avian hosts, mosquito vector, parasites, and environmental conditions that extend across multiple temporal and spatial scales. Prior research, limited in scale, has focused on host-parasite and vector relationships at disparate locations in the islands.

Koloa. Photo courtesy of C.M. Atkinson, USGS.

A holistic modeling approach will be used to study this complex system by integrating across scales ranging from the gene to the landscape. Integrated research projects will focus on demographic studies of exotic and endemic forest birds, mosquito vectors, and pox and malarial parasites using study plots that span a range of climate, hydrology, and vegetation patterns. Complementary laboratory studies will focus on genetic variation of hosts, vectors and parasites and epidemiological factors such as host susceptibility and resistance, parasite virulence and vector competency. Components of the study will be linked through a GIS based modeling approach to incorporate important spatial patterns (e.g., homogeneous vs. fragmented landscapes), spatial complexity, and land use patterns. The model will be used to evaluate broad hypotheses about the dynamics of this system including how biocomplexity associated with biotic and abiotic components of the system at multiple scales affects the persistence of disease in forest bird populations, how changes in land use and environmental conditions affect the stability of the system, and how habitat changes and specific conservation strategies might alter long-term trends in the decline and extinction of the endemic Hawaiian avifauna. An important objective will be to identify weak links and determine the ecological scale that is necessary to facilitate future intervention in this disease system. In addition, specific hypotheses about how parasite virulence, vector susceptibility, and host resistance may be co-evolving in this recent host/parasite/vector association will be investigated.

The proposed study location is on the east flank of Mauna Loa on the island of Hawaii and encompasses major portions of Hawaii Volcanoes National Park, State Natural Area and Forest Reserves, small towns, and rural agricultural areas. Prior ecological studies of this region provide a wealth of background data that can be incorporated into the model. This approach will be applicable to a wide range of conservation issues both in the state of Hawaii and elsewhere in the world.

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